



SEQUENCE LISTING

<110> HONG, GUO FAN
HUANG, WEI-HUA

<120> DNA POLYMERASE HAVING ABILITY TO REDUCE INNATE
SELECTIVE DISCRIMINATION AGAINST FLUORESCENT
DYE-LABELED DIDEOXYNUCLEOTIDES

<130> Lee109

<140> 09/512,019

<141> 2000-02-24

<150> 09/157,397

<151> 1998-09-12

<150> 08/642,684

<151> 1996-05-03

<160> 16

<170> PatentIn Ver. 3.2

<210> 1

<211> 1764

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 1

```
gccgaagggg agaaaaccgct tgaggagatg gagtttgcca tcgttgacgt cattaccgaa 60
gagatgcttg ccgacaaggc agcgccttgc gttgaggtga tggaaagaaaa ctaccacgat 120
gccccgattg tcggaatcgc actagtgaac gagcatgggc gattttttat gcgcccggag 180
accgcgctgg ctgattcgca attttttagca tggccttgccg atgaaacgaa gaaaaaaagc 240
atgtttgacg ccaagcgggc agtcgttgcc ttaaagtga aaggaattga gcttcgcggc 300
gtcgcccttg atttattgct cgctgcctat ttgctcaatc cggctcaaga tgccggcgat 360
atcgctgcgg tggcgaaaat gaaacaatat gaagcgggtgc ggtcggatga agcgggtctat 420
ggcaaaggcg tcaagcgggc gctgccggac gaacagacgc ttgctgagca tctcgttcgc 480
aaagcggcag ccatttgggc gcttgagcag ccgtttatgg acgatttgcg gaacaacgaa 540
caagatcaat tattaacgaa gcttgagcac gcgctggcgg cgattttggc tgaaatggaa 600
ttcactgggg tgaacgtgga taaaaagcgg cttgaacaga tgggttcgga gctcgccgaa 660
caactgcgtg ccacgcagca gcgcatttac gagctagccg gccaaagagt caacattaac 720
tcacaaaaac agctcggagt ctttttattt gaaaagctgc agctaccggt gctgaagaag 780
acgaaaacag gctattcgac ttccggctgat gtgcttgaga agcttgccgc gcatcatgaa 840
atcgtcgaaa acattttgca ttaccgccag cttggcaaac tgcaatcaac gtatattgaa 900
ggattgttga aagttgtgcy ccctgatacc ggcaaagtgc atacgatgtt caaccaagcg 960
ctgacgcaaa ctgggcgggt cagctcggcc gagccgaact tgcaaaacat tccgattcgg 1020
ctcgaagagg ggcggaaaat ccgccaagcg ttcgctccgt cagagccgga ctggctcatt 1080
ttcgccgccc attactcaca aattgaattg cgcgtcctcg cccatatcgc cgatgacgac 1140
aatctaattg aagcgttcca acgcgatttg gatattcaca caaaaacggc gatggacatt 1200
ttccagttga gcgaagagga agtcacggcc aacatgcgcc gccaggcaaa ggccgttaac 1260
ttcggtatcg tttacggaat tagcgattac ggtattggcg aaaacttgaa cattacgcgc 1320
aaagaagctg ccgaatttat cgaacggttac ttccgcagct ttccgggcgt aaagcagtat 1380
atggaaaaca tagtgcaaga agcgaacag aaaggatatg tgacaacgct gttgcatcgg 1440
cgccgctatt tgcctgatat tacaagccgc aatttcaacg tccgcagttt tgcagagcgg 1500
acggccatga acacgccaat tcaaggaagc gccgctgaca ttattaaaaa agcgatgatt 1560
gatttagcgg cacggctgaa agaagagcag cttcaggctc gtcttttgct gcaagtgcatt 1620
gacgagctca ttttggaagc gccaaaagag gaaattgagc gattatgtga gcttggttccg 1680
```

gaagtgatgg agcaggccgt tacgctccgc gtgccgctga aagtcgacta ccattacggc 1740
ccaacatggt atgatgcaa ataa 1764

<210> 2

<211> 587

<212> PRT

<213> Bacillus stearothermophilus

<400> 2

Ala Glu Gly Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Val Asp
1 5 10 15
Val Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val Glu
20 25 30
Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala Leu
35 40 45
Val Asn Glu His Gly Arg Phe Phe Met Arg Pro Glu Thr Ala Leu Ala
50 55 60
Asp Ser Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys Ser
65 70 75 80
Met Phe Asp Ala Lys Arg Ala Val Val Ala Leu Lys Trp Lys Gly Ile
85 90 95
Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu Leu
100 105 110
Asn Pro Ala Gln Asp Ala Gly Asp Ile Ala Ala Val Ala Lys Met Lys
115 120 125
Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly Val
130 135 140
Lys Arg Ser Leu Pro Asp Glu Gln Thr Leu Ala Glu His Leu Val Arg
145 150 155 160
Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp Leu
165 170 175
Arg Asn Asn Glu Gln Asp Gln Leu Leu Thr Lys Leu Glu His Ala Leu
180 185 190
Ala Ala Ile Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp Thr
195 200 205
Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg Ala
210 215 220
Ile Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile Asn
225 230 235 240
Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu Pro
245 250 255

Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val Leu
 260 265 270
 Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His Tyr
 275 280 285
 Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu Lys
 290 295 300
 Val Val Arg Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln Ala
 305 310 315 320
 Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln Asn
 325 330 335
 Ile Pro Ile Arg Leu Glu Glu Gly Arg Lys Ile Arg Gln Ala Phe Val
 340 345 350
 Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln Ile
 355 360 365
 Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile Glu
 370 375 380
 Ala Phe Gln Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp Ile
 385 390 395 400
 Phe Gln Leu Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln Ala
 405 410 415
 Lys Ala Val Asn Phe Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly Leu
 420 425 430
 Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile Glu
 435 440 445
 Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn Ile
 450 455 460
 Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His Arg
 465 470 475 480
 Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg Ser
 485 490 495
 Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala Ala
 500 505 510
 Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys Glu
 515 520 525
 Glu Gln Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu Ile
 530 535 540
 Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Glu Leu Val Pro
 545 550 555 560

Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val Asp
 565 570 575

Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

<210> 3

<211> 1764

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 3

```

atggccgaag gggagaaacc gcttgaggag atggagtttg ccatcgttga cgtcattacc 60
gaagagatgc ttgccgacaa ggcagcgctt gtcgttgagg tgatggaaga aaactaccac 120
gatgccccga ttgtcggaat cgcactagtg aacgagcatg ggcgattttt tatgcgcccg 180
gagaccgcgc tggctgattc gcaattttta gcatggcttg ccgatgaaac gaagaaaaaa 240
agcatgtttg acgccaagcg ggcagtcggt gccttaaagt ggaaaggaat tgagcttcgc 300
ggcgctgcct ttgatttatt gctcgctgcc tatttgctca atccggctca agatgccggc 360
gatatcgctg cgggtggcgaa aatgaaacaa tatgaagcgg tgcggtcgga tgaagcggtc 420
tatggcaaa ggcgtcaagcg gtcgctgccg gacgaacaga cgcttgctga gcatctcggt 480
cgcaaagcgg cagccatttg ggcgcttgag cagccgttta tggacgattt gcggaacaac 540
gaacaagatc aattattaac gaagcttgag cacgcgctgg cggcgatttt ggctgaaatg 600
gaattcactg ggggtgaacgt ggatacaaag cggcttgaac agatgggttc ggagctcgcc 660
gaacaactgc gtgccatcga gcagcgcatc tacgagctag ccggccaaga gttcaacatt 720
aactcaccaa aacagctcgg agtcatttta tttgaaaagc tgcagctacc ggtgctgaag 780
aagacgaaaa caggctattc gacttcggct gatgtgcttg agaagcttgc gccgcatcat 840
gaaatcgctc aaaacatttt gcattaccgc cagcttggca aactgcaatc aacgtatatt 900
gaaggattgt tgaaagtgtg gcgccctgat accggcaaa tgcatacgat gttcaaccaa 960
gcgctgacgc aaactgggcg gctcagctcg gccgagccga acttgcaaaa cattccgatt 1020
cggacccac tggggcgga aatccgccaa gcgttcgtcc cgtcagagcc ggactggctc 1080
attttcgccc cgattactc acaaattgaa ttgcgcgtcc tcgcccatat cgccgatgac 1140
gacaatctaa ttgaagcgtt ccaacgcgat ttggatatcc acacaaaaac ggcgatggac 1200
attttccagt tgagcgaaga ggaagtcacg gccaacatgc gccgccaggc aaaggccggt 1260
aactacggta tcgtttacgg aattagcgat tacggattgg cgcaaaactt gaacattacg 1320
cgcaaagaag ctgccgaatt tatcgacgt tacttcgcca gctttccggg cgtaaagcag 1380
tatatggaaa acatagtgc agaagcgaaa cagaaaggat atgtgacaac gctgttgcat 1440
cggcgccgct atttgcctga tattacaagc cgcaatttca acgtccgcag ttttgcagag 1500
cggacggcca tgaacacgcc aattcaagga agcgccgctg acattattaa aaaagcgatg 1560
attgatttag cggcacggct gaaagaagag cagcttcagg ctgctctttt gctgcaagtg 1620
catgacgagc tcattttgga agcgccaaaa gaggaaattg agcgattatg tgagcttggt 1680
ccggaagtga tggagcaggc cgttacgctc cgcgtgccgc tgaaagtcga ctaccattac 1740
ggcccaacat ggtatgatgc caaa

```

1764

<210> 4

<211> 588

<212> PRT

<213> *Bacillus stearothermophilus*

<400> 4

Met Ala Glu Gly Glu Lys Pro Leu Glu Glu Met Glu Phe Ala Ile Val
 1 5 10 15
 Asp Val Ile Thr Glu Glu Met Leu Ala Asp Lys Ala Ala Leu Val Val
 20 25 30

Glu Val Met Glu Glu Asn Tyr His Asp Ala Pro Ile Val Gly Ile Ala
 35 40 45
 Leu Val Asn Glu His Gly Arg Phe Phe Met Arg Pro Glu Thr Ala Leu
 50 55 60
 Ala Asp Ser Gln Phe Leu Ala Trp Leu Ala Asp Glu Thr Lys Lys Lys
 65 70 75 80
 Ser Met Phe Asp Ala Lys Arg Ala Val Val Ala Leu Lys Trp Lys Gly
 85 90 95
 Ile Glu Leu Arg Gly Val Ala Phe Asp Leu Leu Leu Ala Ala Tyr Leu
 100 105 110
 Leu Asn Pro Ala Gln Asp Ala Gly Asp Ile Ala Ala Val Ala Lys Met
 115 120 125
 Lys Gln Tyr Glu Ala Val Arg Ser Asp Glu Ala Val Tyr Gly Lys Gly
 130 135 140
 Val Lys Arg Ser Leu Pro Asp Glu Gln Thr Leu Ala Glu His Leu Val
 145 150 155 160
 Arg Lys Ala Ala Ala Ile Trp Ala Leu Glu Gln Pro Phe Met Asp Asp
 165 170 175
 Leu Arg Asn Asn Glu Gln Asp Gln Leu Leu Thr Lys Leu Glu His Ala
 180 185 190
 Leu Ala Ala Ile Leu Ala Glu Met Glu Phe Thr Gly Val Asn Val Asp
 195 200 205
 Thr Lys Arg Leu Glu Gln Met Gly Ser Glu Leu Ala Glu Gln Leu Arg
 210 215 220
 Ala Ile Glu Gln Arg Ile Tyr Glu Leu Ala Gly Gln Glu Phe Asn Ile
 225 230 235 240
 Asn Ser Pro Lys Gln Leu Gly Val Ile Leu Phe Glu Lys Leu Gln Leu
 245 250 255
 Pro Val Leu Lys Lys Thr Lys Thr Gly Tyr Ser Thr Ser Ala Asp Val
 260 265 270
 Leu Glu Lys Leu Ala Pro His His Glu Ile Val Glu Asn Ile Leu His
 275 280 285
 Tyr Arg Gln Leu Gly Lys Leu Gln Ser Thr Tyr Ile Glu Gly Leu Leu
 290 295 300
 Lys Val Val Arg Pro Asp Thr Gly Lys Val His Thr Met Phe Asn Gln
 305 310 315 320
 Ala Leu Thr Gln Thr Gly Arg Leu Ser Ser Ala Glu Pro Asn Leu Gln
 325 330 335

Asn Ile Pro Ile Arg Thr Pro Leu Gly Arg Lys Ile Arg Gln Ala Phe
 340 345 350
 Val Pro Ser Glu Pro Asp Trp Leu Ile Phe Ala Ala Asp Tyr Ser Gln
 355 360 365
 Ile Glu Leu Arg Val Leu Ala His Ile Ala Asp Asp Asp Asn Leu Ile
 370 375 380
 Glu Ala Phe Gln Arg Asp Leu Asp Ile His Thr Lys Thr Ala Met Asp
 385 390 395 400
 Ile Phe Gln Leu Ser Glu Glu Glu Val Thr Ala Asn Met Arg Arg Gln
 405 410 415
 Ala Lys Ala Val Asn Tyr Gly Ile Val Tyr Gly Ile Ser Asp Tyr Gly
 420 425 430
 Leu Ala Gln Asn Leu Asn Ile Thr Arg Lys Glu Ala Ala Glu Phe Ile
 435 440 445
 Glu Arg Tyr Phe Ala Ser Phe Pro Gly Val Lys Gln Tyr Met Glu Asn
 450 455 460
 Ile Val Gln Glu Ala Lys Gln Lys Gly Tyr Val Thr Thr Leu Leu His
 465 470 475 480
 Arg Arg Arg Tyr Leu Pro Asp Ile Thr Ser Arg Asn Phe Asn Val Arg
 485 490 495
 Ser Phe Ala Glu Arg Thr Ala Met Asn Thr Pro Ile Gln Gly Ser Ala
 500 505 510
 Ala Asp Ile Ile Lys Lys Ala Met Ile Asp Leu Ala Ala Arg Leu Lys
 515 520 525
 Glu Glu Gln Leu Gln Ala Arg Leu Leu Leu Gln Val His Asp Glu Leu
 530 535 540
 Ile Leu Glu Ala Pro Lys Glu Glu Ile Glu Arg Leu Cys Glu Leu Val
 545 550 555 560
 Pro Glu Val Met Glu Gln Ala Val Thr Leu Arg Val Pro Leu Lys Val
 565 570 575
 Asp Tyr His Tyr Gly Pro Thr Trp Tyr Asp Ala Lys
 580 585

<210> 5

<211> 17

<212> DNA

<213> *Bacillus stearothermophilus*

<400> 5

cattttgctg ccggtca

<210> 6
 <211> 20
 <212> DNA
 <213> *Bacillus stearothermophilus*

 <400> 6
 gtaaaacgac ggccagtctt 20

<210> 7
 <211> 20
 <212> DNA
 <213> *Bacillus stearothermophilus*

 <400> 7
 gtaaaacgac ggccagtcgg 20

<210> 8
 <211> 20
 <212> DNA
 <213> *Bacillus stearothermophilus*

 <400> 8
 cattttgctg ccggtcagaa 20

<210> 9
 <211> 26
 <212> DNA
 <213> *Bacillus stearothermophilus*

 <400> 9
 gccgttaact acggtatcgt ttacgg 26

<210> 10
 <211> 36
 <212> DNA
 <213> *Bacillus stearothermophilus*

 <400> 10
 cattccgatt cggacccac tggggcggaa aatccg 36

<210> 11
 <211> 24
 <212> DNA
 <213> *Bacillus stearothermophilus*

 <400> 11
 ssssstgta aaacgacggc cagt 24

<210> 12
 <211> 743
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Template DNA
 sequence

<220>
 <221> modified_base
 <222> (669)
 <223> a, c, g, t, other or unknown

<400> 12
 ctcaactatag ggcgaattcg agctcgggtac ccggggatcc tctagagtcg acctgcaggc 60
 atgcaagctt gaggatttcta tagtgtcacc taaatagctt ggcgtaatca tgggtcatagc 120
 tgtttcctgt gtgaaattgt tatccgctca caattccaca caacatacga gccggaagca 180
 taaagtgtaa agcctgggggt gcctaattgag tgagctaaact cacattaatt gcgttgcgct 240
 cactgcccgc tttgcagtcg ggaaacctgt cgtgccagct gcattaatga atcggccaac 300
 gcgcggggag aggcgggtttg cgtattgggc gctcttcgcg ttctctcgctc actgactcgc 360
 tgcgctcgggt cgttcgggctg cggcgagcgg tatcagctca ctcaaaggcg gtaatacgggt 420
 tatccacaga atcaggggat aacgcaggaa agaacatgtg agcaaaaggc cagcaaaagg 480
 ccaggaaccg taaaaaggcc gcgttgctgg cgtttttcca taggctccgc cccctgacg 540
 agcatcacaa aaatcgacgc tcaagtcaga ggtggcgaaa cccgacagga ctataaagat 600
 accaggcgtt tccccctgga agctccctcg tgcgctctcc tgttccgaac cctgccgctt 660
 accggatanc tgtccgcctt ttctcttcgg aaagcgtggc gtttctcata agctcacgtg 720
 taggtattct cagttcgggtt agc 743

<210> 13
 <211> 657
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Template DNA
 sequence

<220>
 <221> modified_base
 <222> (611)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (618)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (622)..(623)
 <223> a, c, g, t, other or unknown

<400> 13
 atgcctgcag gtcgactcta gaggatcccc gggtaccgag ctccaattcg taatcatgggt 60
 catagctgtt tcctgtgtga aattgttata cgctcacaaat tccacacaaac atacgagccg 120
 gaagcataaaa gtgtaaagcc tgggggtgcct aatgagtgag ctaactcaca ttaattgcgt 180
 tgcgctcact gcccgccttcc cagtcgggaa acctgtcgtg ccagcctgca ttaatgaatc 240
 ggccaacgcg cggggagagg cggtttgcgt attgggcgcc aggggtggtt ttcttttcac 300
 cagtgcagacg ggcaacagct gattgccctt caccgcctgg ccctgagaga gttgcagcaa 360
 gcgggtccacg ctgggtttgcc ccagcaggcg aaaatcctgt ttgatgggtg ttccgaaatc 420


```

ggcaaaatcc cttataaatc aaaagaatag cccgagatag ggttgagtgt tgttccagtt 480
tggaacaaga gtccactatt aaagaacgtg gactccaacg tcaaagggcg aaaaaccgtc 540
tatcagggcg atggccacta cgtgaaccat caccctaaatc aagttttttg gggtcgaggt 600
gccgtaaagc nctaaatngg annctaaag ggagcccccg atttagagct tgacggg 657

```

```

<210> 14
<211> 672
<212> DNA
<213> Unknown Organism

```

```

<220>
<223> Description of Unknown Organism: Template DNA
      sequence

```

```

<220>
<221> modified_base
<222> (9)
<223> a, c, g, t, other or unknown

```

```

<220>
<221> modified_base
<222> (27)
<223> a, c, g, t, other or unknown

```

```

<220>
<221> modified_base
<222> (41)
<223> a, c, g, t, other or unknown

```

```

<220>
<221> modified_base
<222> (50)
<223> a, c, g, t, other or unknown

```

```

<220>
<221> modified_base
<222> (55)
<223> a, c, g, t, other or unknown

```

```

<220>
<221> modified_base
<222> (59)
<223> a, c, g, t, other or unknown

```

```

<220>
<221> modified_base
<222> (63)
<223> a, c, g, t, other or unknown

```

```

<220>
<221> modified_base
<222> (71)
<223> a, c, g, t, other or unknown

```

<220>
<221> modified_base
<222> (75)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (92)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (101)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (106)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (123)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (150)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (164)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (173)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (175)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (179)..(180)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (182)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (205)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (212)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (216)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (222)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (235)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (240)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (242)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (249)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (253)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (266)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (278)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (282)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (285)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (305)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (312)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (314)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (317)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (333)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (335)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (343)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (351)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (355)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (366)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (368)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (381)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (384)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (387)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (389)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (391)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (404)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (446)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (467)
<223> a, c, g, t, other or unknown

<220>
<221> modified_base
<222> (490)
<223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (563)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (590)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (597)
 <223> a, c, g, t, other or unknown

<400> 14
 ttgatattgnt catatagggg gtttcgngtc ggtaccgggg ntcctctagn gtcgnectgna 60
 ggnatgcaag nttgngtatt ctatagtgtc anctaaatag nttggngtaa tcatgggtcat 120
 agntgtttcc tgtgtgaaat tgttatccgn tcacaattcc acanaaaaata cgngnecggnn 180
 gnataaagt taaagcctgg ggtgnctaata gngtgngtta antcacatta attgngttgn 240
 gntcaatgnc cgntttccag tcgggnaacc tgcgtgnca gntgnattaa tgggttcggcc 300
 aacgngcggg gngnggnggt ttgggtattg ggngntcttc cgnttcctcg ntcantgatt 360
 cgttgngntc ggtcgttcgg ntgnggngng nggtatcaga tcantcaaag ggggtaatac 420
 ggttatccac agaatacagg ggtangggag gtaaggacat gtggggnaaa agggcagcaa 480
 aagggcaggn accgtaaaaa ggccggttg tgggggttt tccatagggt ccgccccct 540
 gggggggatc aaaaaaatc cgnggccaaag tcaaggggtg gggggaccn ccagggnnta 600
 taaagggtacc aggggttccc cctgggagtc cctcgtggg tctcctgtcc gccctgcccc 660
 ttaccgggta ct 672

<210> 15
 <211> 686
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Template DNA
 sequence

<220>
 <221> modified_base
 <222> (561)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (656)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (678)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (680)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (682)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (685)
 <223> a, c, g, t, other or unknown

<400> 15
 acgagctcga attcgtaatc atgggtcatag ctgtttcctg tgtgaaattg ttatccgctc 60
 acaattccac acaacatacg agccggaagc ataaagtgtg aagcctgggg tgccaatgag 120
 tgagctaact cacattaatt gcgttgcgct cactgcccgc tttccagtcg ggaaacctgt 180
 cgtgccagct gcattaatga atcggccaac gcgcggggag aggcgggttg cgtattgggc 240
 gccagggtgg tttttctttt caccagttag acgggcaaca gctggattgc ccttcaccgc 300
 ctggccctga gagagttaga gcaagcgggc cacgctgggt tgccccagca ggcgaaaatc 360
 ctgtttgatg gtggttccga aatcggcaaa atcccttata aatcaaaaga ataggccgag 420
 atagggttga gtgttgttcc agtttgggaa aagagtccac tattaagaa cgtggactcc 480
 aacgtcaaag ggcgaaaaac cgtctatcag ggcgatgcca ctacgtgaac catcacccaa 540
 atcaagtttt ttgggggtcga ngttgccgta aagcattaaa tcgggaacct aaaggagacc 600
 ccgatttaga gcttgagggg gaaagccggc gaacgtgggc gagaaaaagg aggggnagaa 660
 accgaaagga gcggcctnan gncgng 686

<210> 16
 <211> 673
 <212> DNA
 <213> Unknown Organism

<220>
 <223> Description of Unknown Organism: Template DNA
 sequence

<220>
 <221> modified_base
 <222> (9)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (27)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (41)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (468)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (491)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (564)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (591)
 <223> a, c, g, t, other or unknown

<220>
 <221> modified_base
 <222> (598)
 <223> a, c, g, t, other or unknown

<400> 16
 ttgatatgnt catatagggg gtttcgngtc ggtaccgggg ntcctctaga gtcgacctgc 60
 aggcattgcaa gcttgagtat tctatagtgt cacctaaata gcttggcgta atcatggtca 120
 tagctgtttc ctgtgtgaaa ttgttatccg ctcaaatc cacacaacat acgagccgga 180
 agcataaagt gtaaagcctg ggggtgcctaa tgagttagct aactcacatt aattgcgttg 240
 cgctcactgc ccgctttcca gtcgggaaac ctgtcgtgcc agctgcatta atgaatcggc 300
 caacgcgcgg ggagaggcgg ttgcggtatt gggcgctctt ccgcttcctc gctcactgac 360
 tcgctgcgct cggctcgttcg gctgcggcgc gcggtatcag ctactcaaa ggcggtaata 420
 cggttatcca cagaatcagg ggataacgga ggtaaggaca tgtggggnaa aagggcagca 480
 aaagggcagg naccgtaaaa aggcgggttg gttggggttt ttccataggg tccgcccccc 540
 tgggggggat caaaaaaaaaa ccgnggccaa gtcaaggggt ggggggacct nccagggntt 600
 ataaagggtac caggggttcc ccctgggagt ccctcgtgg gtctcctgtc cgccctgccc 660
 gttacccggt act 673